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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 07:48:26 ; Search time 100 Seconds
(without alignments)
210.958 Million cell updates/sec

Title: PCT-US03-05305-4

Perfect score: 21
Sequence: 1 cagcagcagagcttcatcat 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 639749 seqs, 502280978 residues

Total number of hits satisfying chosen parameters: 377018

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA:

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq*
- 4: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq*
- 5: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	10	US-09-944-326-4
2	14.8	70.5	21	10	US-09-944-326-1
3	14.8	70.5	21	10	US-09-944-326-2
C 4	14.8	70.5	31	9	US-10-196-107A-35
C 5	14.8	70.5	31	10	US-09-374-671-35
C 6	14.2	67.6	22	9	US-10-006-856A-163
C 7	14.2	67.6	22	9	US-10-006-818A-163
C 8	14.2	67.6	22	9	US-10-015-393A-163
C 9	14.2	67.6	26	9	US-10-006-856A-164
C 10	14.2	67.6	26	9	US-10-006-818A-164
C 11	14.2	67.6	26	9	US-10-015-393A-164
C 12	13.8	65.7	28	9	US-09-864-364-3
C 13	13.8	65.7	37	10	US-10-196-107A-54
C 14	13.8	65.7	37	10	US-09-374-671-54
C 15	13.6	64.8	24	10	US-09-939-709-3
C 16	13.6	64.8	49	9	US-09-805-353-19
C 17	13.6	64.8	50	9	US-09-992-598-312
C 18	13.6	64.8	50	9	US-09-989-293A-312
C 19	13.6	64.8	50	9	US-09-989-735-312

20	13.6	64.8	50	9	US-09-990-444-312	Sequence 312, App
21	13.6	64.8	50	9	US-09-989-730-312	Sequence 312, App
22	13.6	64.8	50	9	US-09-990-436-312	Sequence 312, App
23	13.6	64.8	50	9	US-09-991-181-312	Sequence 312, App
24	13.6	64.8	50	9	US-09-993-687-312	Sequence 312, App
25	13.6	64.8	50	9	US-09-989-734-312	Sequence 312, App
26	13.6	64.8	50	9	US-09-997-653-312	Sequence 312, App
27	13.6	64.8	50	9	US-09-993-667-312	Sequence 312, App
28	13.6	64.8	50	9	US-09-990-438-312	Sequence 312, App
29	13.6	64.8	50	9	US-09-990-562-312	Sequence 312, App
30	13.6	64.8	50	9	US-09-997-428-312	Sequence 312, App
31	13.6	64.8	50	9	US-09-997-666-312	Sequence 312, App
32	13.6	64.8	50	9	US-09-990-711-312	Sequence 312, App
33	13.6	64.8	50	9	US-09-989-726-312	Sequence 312, App
34	13.6	64.8	50	9	US-09-990-437-312	Sequence 312, App
35	13.6	64.8	50	9	US-09-998-156-312	Sequence 312, App
36	13.6	64.8	50	9	US-09-991-157-312	Sequence 312, App
37	13.6	64.8	50	9	US-09-991-172-312	Sequence 312, App
38	13.6	64.8	50	9	US-09-997-514-312	Sequence 312, App
39	13.6	64.8	50	9	US-09-997-573-312	Sequence 312, App
40	13.6	64.8	50	9	US-09-990-443-312	Sequence 312, App
41	13.6	64.8	50	9	US-09-990-726-312	Sequence 312, App
42	13.6	64.8	50	9	US-09-997-559-312	Sequence 312, App
43	13.6	64.8	50	9	US-09-997-601-312	Sequence 312, App
44	13.6	64.8	50	9	US-09-989-729A-312	Sequence 312, App
45	13.6	64.8	50	9	US-09-990-440-312	Sequence 312, App

ALIGNMENTS

RESULT 1
US-09-944-326-4
; Sequence 4, Application US/09944326
; Patent No. US20020128220A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY
; FILE REFERENCE: UBC.P-020-2
; CURRENT APPLICATION NUMBER: US/09/944,326
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-09-944-326-4
Query Match 100.0%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAGCAGCAGAGCTTTCATCAT 21
Db 1 CAGCAGCAGAGCTTTCATCAT 21
RESULT 2
US-09-944-326-1
; Sequence 1, Application US/09944326
; Patent No. US20020128220A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin

; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY
; FILE REFERENCE: UBC.P-020-2
; CURRENT APPLICATION NUMBER: US/09/944,326
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-09-944-326-1

Query Match 70.5%; Score 14.8; DB 10; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCAT 18
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Db 4 CAGCAGGAGAGTCTTCAT 21

RESULT 3
US-09-944-326-2
; Sequence 2, Application US/09944326
; Patent No. US20020128220A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY
; FILE REFERENCE: UBC.P-020-2
; CURRENT APPLICATION NUMBER: US/09/944,326
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: mismatch control
US-09-944-326-2

Query Match 70.5%; Score 14.8; DB 10; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCAT 18
||||| ||| |||||
Db 4 CAGCAGGAGAGTCTTCAT 21

RESULT 4
US-10-196-107A-35/c
; Sequence 35, Application US/10196107A
; Publication No. US20030049691A1
; GENERAL INFORMATION:
; APPLICANT: Morgenstern, Jay P.
; APPLICANT: Konieczny, Andrzej

; Bizindauskas, Christine B.
; Brauer, Andrew W.
; TITLE OF INVENTION: Allergenic Protein and Peptides from Dog
; Dander and Uses Therefor
; NUMBER OF SEQUENCES: 109
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/196,107A
; FILING DATE: 16-Jul-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/374,671
; FILING DATE: 1999-AUG-16
; APPLICATION NUMBER: US 08/491,861
; FILING DATE: 1995-OCT-27
; APPLICATION NUMBER: PCT/US93/12468
; FILING DATE: 1993-DEC-30
; APPLICATION NUMBER: US 08/156,549
; FILING DATE: 1993-NOV-22
; APPLICATION NUMBER: US 07/999,712
; FILING DATE: 1992-DEC-31
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiorgio, Jeanne M.
; REGISTRATION NUMBER: 41,710
; REFERENCE/DOCKET NUMBER: IMI-026C2CNCPADV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-10-196-107A-35

Query Match 70.5%; Score 14.8; DB 9; Length 31;
Best Local Similarity 88.9%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AGCAGCAGAGTCTTCATC 19
||||| |||||
Db 24 AGGAGCAGGAGTCTTCATC 7

RESULT 5
US-09-374-671-35/c
; Sequence 35, Application US/09374671
; Patent No. US20020012963A1
; GENERAL INFORMATION:
; APPLICANT: Morgenstern, Jay P.
; APPLICANT: Kanieczny, Andrzej
; APPLICANT: Bizindauskas, Christine B.
; APPLICANT: Brauer, Andrew W.
; TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog
; Dander and Uses Therefor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston

STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII-text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/374,671
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/491,861
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-026CP(IPC-048CP)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-374-671-35

Query Match 70.5%; Score 14.8; DB 10; Length 31;
Best Local Similarity 88.9%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCAGCAGAGTCTTTCATC 19
Db 24 AGCAGCAGGGTCTTTCATC 7

RESULT 6
US-10-006-856A-163/c
; Sequence 163, Application US/10006856A
; Publication No. US2003004841A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C14
; CURRENT APPLICATION NUMBER: US/10/006,856A
; CURRENT FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 477
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 163
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-856A-163

Query Match 67.6%; Score 14.2; DB 9; Length 22;
Best Local Similarity 84.2%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTTCATC 19
Db 22 CAGGACAGGGTCTTTCATC 4

RESULT 7
US-10-006-818A-163/c
; Sequence 163, Application US/10006818A
; Publication No. US20030054406A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C14
; CURRENT APPLICATION NUMBER: US/10/006,818A
; CURRENT FILING DATE: 2001-12-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 163
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-818A-163

Query Match 67.6%; Score 14.2; DB 9; Length 22;
Best Local Similarity 84.2%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTTCATC 19
Db 22 CAGGACAGGGTCTTTCATC 4

RESULT 8
US-10-015-393A-163/c
; Sequence 163, Application US/10015393A
; Publication No. US20030069179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
US-10-006-856A-163

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; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PlC46
; CURRENT APPLICATION NUMBER: US/10/015.393A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 163
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-393A-163
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```
Query Match          67.6%; Score 14.2; DB 9; Length 22;
Best Local Similarity 84.2%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy 1 CAGCAGCAGAGTCTTCATC 19
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Db 22 CAGGAACAGGGTCTTCATC 4
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RESULT 9

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US-10-006-856A-164/c
; Sequence 164, Application US/10006856A
; Publication No. US20030044841A1
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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PlC14
; CURRENT APPLICATION NUMBER: US/10/006.856A
; CURRENT FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 477
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 164
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-856A-164
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Query Match          67.6%; Score 14.2; DB 9; Length 26;
Best Local Similarity 84.2%; Pred. No. 9.6e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy 1 CAGCAGCAGAGTCTTCATC 19
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Db 22 CAGGAACAGGGTCTTCATC 4
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RESULT 10

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US-10-006-818A-164/c
; Sequence 164, Application US/10006818A
; Publication No. US20030054406A1
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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
```

```
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PlC4
; CURRENT APPLICATION NUMBER: US/10/006.818A
; CURRENT FILING DATE: 2001-12-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 164
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-818A-164
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Query Match          67.6%; Score 14.2; DB 9; Length 26;
Best Local Similarity 84.2%; Pred. No. 9.6e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy 1 CAGCAGCAGAGTCTTCATC 19
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Db 22 CAGGAACAGGGTCTTCATC 4
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RESULT 11

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US-10-015-393A-164/c
; Sequence 164, Application US/10015393A
; Publication No. US20030069179A1
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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PlC46
; CURRENT APPLICATION NUMBER: US/10/015.393A
; CURRENT FILING DATE: 2002-08-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 164
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-393A-164
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Query Match          67.6%; Score 14.2; DB 9; Length 26;
Best Local Similarity 84.2%; Pred. No. 9.6e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 CAGCAGCAGGCTTCATC 19
||| | ||| ||||| |||
Db 22 CAGGAACAGGCTTCATC 4

RESULT 12
US-09-864-364-3/c
; Sequence 3, Application US/09864364
; Publication No. US20030005470A1
; GENERAL INFORMATION:
; APPLICANT: CHUGAISEIYAKU KABUSIKIGAISYA
; TITLE OF INVENTION: NO. US20030005470A1-Human Animal Exhibiting Bone Metastasis Of Tu
; FILE REFERENCE: PH-1182US
; CURRENT APPLICATION NUMBER: US/09/864,364
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: JP 2001-140538
; PRIOR FILING DATE: 2001-05-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 3
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: IL-11 primer
US-09-864-364-3

Query Match 65.7%; Score 13.8; DB 9; Length 28;
Best Local Similarity 88.2%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CAGCAGGCTTCATCA 20
|||| ||||| ||||| ||
Db 25 CAGCCGAGCTTCAGCA 9

RESULT 13
US-10-196-107A-54/c
; Sequence 54, Application US/10196107A
; Publication No. US20030049691A1
; GENERAL INFORMATION:
; APPLICANT: Morgenstern, Jay P.
; Koniczny, Andrzej
; Bizindaukas, Christine B.
; Brauer, Andrew W.
; TITLE OF INVENTION: Allergenic Protein and Peptides from Dog
; Dander and Uses Therefor
; NUMBER OF SEQUENCES: 109
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/196,107A
; FILING DATE: 16-Jul-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/374,671
; FILING DATE: 1999-AUG-16
; APPLICATION NUMBER: US 08/491,861
; FILING DATE: 1995-OCT-27
; APPLICATION NUMBER: PCT/US93/12468
; FILING DATE: 1993-DEC-30
; APPLICATION NUMBER: US 08/156,549
; FILING DATE: 1993-NOV-22

; APPLICATION NUMBER: US 07/999,712
; FILING DATE: 1992-DEC-31
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiorgio, Jeanne M.
; REGISTRATION NUMBER: 41,710
; REFERENCE/DOCKET NUMBER: IMI-026C2CNCPADV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 54:
US-10-196-107A-54

Query Match 65.7%; Score 13.8; DB 9; Length 37;
Best Local Similarity 88.2%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCAGCAGGCTTCAT 18
|| |||| ||||| |||
Db 30 AGGAGCAGGCTTCAT 14

RESULT 14
US-09-374-671-54/c
; Sequence 54, Application US/09374671
; Patent No. US20020012963A1
; GENERAL INFORMATION:
; APPLICANT: Morgenstern, Jay P.
; APPLICANT: Koniczny, Andrzej
; APPLICANT: Bizindaukas, Christine B.
; APPLICANT: Brauer, Andrew W.
; TITLE OF INVENTION: Allergenic proteins and peptides from Dog
; Dander and Uses Therefor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/374,671
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/491,861
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-026C1P-048CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA

US-09-374-671-54

Query Match 65.7%; Score 13.8; DB 10; Length 37;
 Best Local Similarity 88.2%; Pred. No. 1.6e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCAGCAGAGTCTTCAT 18
 || ||||| |||||
 Db 30 AGGAGCAGGGTCTTCAT 14

RESULT 15

US-09-939-709-3
 ; Sequence 3, Application US/09939709
 ; Patent No. US2002007273A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BARON, Roland E.
 ; APPLICANT: SIMS, Natalie
 ; APPLICANT: SABATAKOS, Georgios
 ; APPLICANT: NESTLER, Eric
 ; APPLICANT: CHEN, Jingshan
 ; APPLICANT: KELZ, Max
 ; TITLE OF INVENTION: Methods of Using Agents that Modulate Bone Formation and Inhibit
 ; FILE OF INVENTION: Adipogenesis
 ; FILE REFERENCE: 044574-5045-US
 ; CURRENT APPLICATION NUMBER: US/09/939,709
 ; CURRENT FILING DATE: 2001-08-28
 ; PRIOR APPLICATION NUMBER: US 60/228,450
 ; PRIOR FILING DATE: 2000-08-29
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 24
 ; TYPE: DNA
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic oligonucleotide: SV40 primer
 US-09-939-709-3

Query Match 64.8%; Score 13.6; DB 10; Length 24;
 Best Local Similarity 80.0%; Pred. No. 1.8e+03;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCA 20
 ||||| || || |||||
 Db 3 CAGCAGTAGCCTCATCA 22

Search completed: April 18, 2003, 08:58:39
 Job time : 108 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 07:44:37 ; Search time 1679 Seconds
(without alignments)
202.564 Million cell updates/sec

Title: PCT-US03-05305-4

Perfect score: 21

Sequence: 1 cagcagcaggtcttcattcatc 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_estl:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	14.8	70.5	46	9	AA916352 oh80ell.s
C 2	14.6	69.5	44	14	W25663 zc64e08.r1
C 3	14	66.7	50	17	BH861678 SALK_0877
4	13	61.9	21	17	AZ802584 2M0061105
5	13	61.9	43	9	AA973632 oo48b04.s
6	12.8	61.0	46	9	AL649065 AL649065

7	12.8	61.0	50	9	AU107924
8	12.8	61.0	50	9	AU107925
9	12.8	61.0	50	9	AU107928
10	12.8	61.0	50	9	AU107929
C 11	12.6	60.0	39	17	AL760945
C 12	12.6	60.0	43	9	AA766391
C 13	12.6	60.0	46	9	AA561123
C 14	12.6	60.0	40	9	AA561123
C 15	12.6	60.0	50	9	AU105963
C 16	12.6	60.0	50	9	AU105967
C 17	12.6	60.0	50	9	AU105968
C 18	12.6	60.0	50	9	AU105972
C 19	12.4	59.0	37	17	AZ797149
C 20	12.2	58.1	35	17	AZ332831
C 21	12.2	58.1	43	17	AZ610505
C 22	12.2	58.1	46	9	AA109083
C 23	12.2	58.1	49	9	AA052336
C 24	12.2	58.1	49	9	AA864073
C 25	12.2	58.1	50	9	AU104442
C 26	12	57.1	33	17	AZ305164
C 27	12	57.1	33	17	AZ318599
C 28	12	57.1	34	9	AA116347
C 29	12	57.1	34	13	BI246596
C 30	12	57.1	46	14	H92446
C 31	12	57.1	46	14	T74174
C 32	12	57.1	47	17	AZ772648
C 33	12	57.1	49	9	AI197165
C 34	12	57.1	49	17	AQ025388
C 35	12	57.1	50	9	AU103332
C 36	12	57.1	50	9	AU103352
C 37	12	57.1	50	9	AU107277
C 38	11.8	56.2	21	17	AZ848076
C 39	11.8	56.2	26	17	AZ600116
C 40	11.8	56.2	37	9	AA079070
C 41	11.8	56.2	38	17	AZ815373
C 42	11.8	56.2	50	9	AU105966
C 43	11.8	56.2	50	9	AU106538
C 44	11.6	55.2	40	9	AA725970
C 45	11.6	55.2	41	17	AL760282

ALIGNMENTS

RESULT 1
AA916352
LOCUS oh80ell.s1 NCI-CGAP_C08 Homo sapiens cDNA clone IMAGE:1473356 3'
DEFINITION similar to TR:Q15347 Q15347 RAGA. [1] ; mRNA sequence.
ACCESSION AA916352
VERSION AA916352.1 GI:3055744
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 46)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
Cloned by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality

AU107924	AU107924
AU107925	AU107925
AU107928	AU107928
AU107929	AU107929
AL760945	Arabidops
AA766391	wh61d04.x
AA561123	v141c01.r
AU105963	AU105963
AU105967	AU105967
AU105968	AU105968
AU105972	AU105972
AA566984	1038 L0d1
AZ797149	2M0053009
AZ332831	1M0061C05
AZ610505	1M0435N18
AA109083	mp37b05.r
AA052336	mb35b02.r
AA864073	vx88f02.r
AU104442	AU104442
AZ305164	1M0005M08
AZ318599	1M0037N24
AA116347	mq70g12.r
BI246596	602958318
H92446	yt89b09.r1
T74174	yc60b12.s1
AZ772648	1M0583N12
AI197165	ue52g02.r
AQ025388	EP(X)1109
AU103332	AU103332
AU103352	AU103352
AU107277	AU107277
AZ848076	2M0148T14
AZ600116	1M0418K16
AA079070	zm93a02.s
AZ815373	2M0083M06
AU105966	AU105966
AU106538	AU106538
AA725970	vu83g12.r
AL760282	Arabidops

QY 3 GCAGCAGAGTCTTC 16
 Db 41 GCAGCAGAGTCTTC 28

RESULT 4

LOCUS AZ802584 21 bp DNA linear GSS 16-FEB-2001
 DEFINITION 2M061105R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0061105 R, DNA sequence.

ACCESSION AZ802584
 VERSION AZ802584.1 GI:12954907
 KEYWORDS GSS.
 SOURCE house mouse.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
 and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

COMMENT Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0061 row: 1 column: 05

Seq primer: CACAGAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

FEATURES

source

1..21

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0061105"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD420v; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|47321141gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 8 a 7 c 3 g

ORIGIN

Query Match 61.9%; Score 13; DB 17; Length 21;
 Best Local Similarity 76.2%; Pred. No. 3e+04;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
 Db 1 CAGCAGCAGCATACATCAT 21

RESULT 5

LOCUS AA973632 43 bp mRNA linear EST 17-JUN-1998
 DEFINITION 0048004.s1 NCI-CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1569391 3',
 similar to SW_XPE_CERAE P33194 POSSIBLE DNA-REPAIR PROTEIN XP-E ;,
 mRNA sequence.

ACCESSION AA973632
 VERSION AA973632.1 GI:3148812
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS 1 (bases 1 to 43)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL

COMMENT Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 703 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1..43

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1569391"

/clone_lib="NCI-CGAP_Lu5"

/tissue_type="carcinoid"

/lab_host="DH10B"

/note="Organ: lung; Vector: p7T73D-Pac (Pharmacia) with a
 modified polylinker; 1st strand cDNA was prepared from
 neuroendocrine lung carcinoid, and was then primed with a
 Not I - oligo(dT) primer. Double-stranded cDNA was ligated
 to Eco RI adaptors (Pharmacia), digested with Not I and
 cloned into the Not I and Eco RI sites of the modified
 p7T73 vector. Library is normalized. Library was
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 15 a 13 c 6 g 9 t

ORIGIN

Query Match 61.9%; Score 13; DB 9; Length 43;
 Best Local Similarity 76.2%; Pred. No. 4.4e+04;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21

Db 1 CAACAATAGAGTCTTCACCAT 21

RESULT 6

LOCUS AL649065 46 bp mRNA linear EST 13-DEC-2001

DEFINITION AL649065 XCC-gastrula Silurana tropicalis cDNA clone IGas034101 5',
 mRNA sequence.

ACCESSION AL649065

VERSION AL649065.1 GI:17658059

BASE COUNT

ORIGIN

Query Match 61.9%; Score 13; DB 9; Length 43;
 Best Local Similarity 76.2%; Pred. No. 4.4e+04;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21

Db 1 CAACAATAGAGTCTTCACCAT 21

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KEYWORDS
SOURCE      EST.
ORGANISM    Silurana tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
            Xenopodinae; Silurana.
REFERENCE   1 (bases 1 to 46)
AUTHORS    Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.
TITLE      Sanger Xenopus tropicalis EST project 2001 (10_2001)
JOURNAL    Unpublished (2001)
COMMENT    Contact: Huckle E
            Sanger Centre
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: tropesanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: Tgas034101.sp6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
FEATURES   Location/Qualifiers
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            1..46
            /organism="Silurana tropicalis"
            /db_xref="taxon:8364"
            /clone_lib="Tgas034101"
            /dev_stage="gastrula (stages 10.5-13 mixed)"
            /lab_host="Escherichia coli XL1-blue"
            /note="Vector: PCS107; Site_1: EcoRI; Site_2: NotI; cDNA
            was oligo dT primed from 5ug of poly A+ RNA from stages
            10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
            into PCS107 with EcoRI at the 5' end and NotI at the 3'
            end."
BASE COUNT      10 a      14 c      11 g      11 t
ORIGIN
Query Match      61.0%; Score 12.8; DB 9; Length 46;
Best Local Similarity 87.5%; Pred. No. 5.6e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 GCAGAGTCTTCATCAT 21
    ||| ||||| |||||
Db 21 GCCGCGTTCATCAT 36

RESULT 7
AUI07924
LOCUS       AUI07924 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HRC02185, mRNA sequence.
ACCESSION  AUI07924
VERSION    AUI07924.1 GI:13557446
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 50)
AUTHORS    Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
            H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
            Y., Nakamura, Y., Suyama, A. and Sugano, S.
            Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
            JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
            S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
BASE COUNT      10 a      14 c      11 g      11 t
ORIGIN
Query Match      61.0%; Score 12.8; DB 9; Length 46;
Best Local Similarity 87.5%; Pred. No. 5.6e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 GCAGAGTCTTCATCAT 21
    ||| ||||| |||||
Db 21 GCCGCGTTCATCAT 36

RESULT 7
AUI07924
LOCUS       AUI07924 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HRC02185, mRNA sequence.
ACCESSION  AUI07924
VERSION    AUI07924.1 GI:13557446
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 50)
AUTHORS    Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
            H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
            Y., Nakamura, Y., Suyama, A. and Sugano, S.
            Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
            JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
            S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES   Location/Qualifiers
            source
            1..50
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="Sugano Homo sapiens cDNA library"
            /note="Differential display comparison of untreated and
            dimethylformate treated U937 cells"
BASE COUNT      10 a      15 c      19 g      6 t
ORIGIN
Query Match      61.0%; Score 12.8; DB 9; Length 50;
Best Local Similarity 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 AGCAGCAGAGTCTTCA 17
    ||||| ||||| ||
Db 27 AGCAGCAGAGTCCGCA 42

RESULT 9
AUI07928
LOCUS       AUI07928 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION ZR62348, mRNA sequence.
ACCESSION  AUI07928

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1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HRC02185"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylformate treated U937 cells"
BASE COUNT      10 a      15 c      21 g      4 t
ORIGIN
Query Match      61.0%; Score 12.8; DB 9; Length 50;
Best Local Similarity 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 AGCAGCAGAGTCTTCA 17
    ||||| ||||| ||
Db 27 AGCAGCAGAGTCCGCA 42

RESULT 8
AUI07925
LOCUS       AUI07925 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HSI06916, mRNA sequence.
ACCESSION  AUI07925
VERSION    AUI07925.1 GI:13557447
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 50)
AUTHORS    Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
            H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
            Y., Nakamura, Y., Suyama, A. and Sugano, S.
            Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
            JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
            S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES   Location/Qualifiers
            source
            1..50
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="Sugano Homo sapiens cDNA library"
            /note="Differential display comparison of untreated and
            dimethylformate treated U937 cells"
BASE COUNT      10 a      15 c      19 g      6 t
ORIGIN
Query Match      61.0%; Score 12.8; DB 9; Length 50;
Best Local Similarity 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 AGCAGCAGAGTCTTCA 17
    ||||| ||||| ||
Db 27 AGCAGCAGAGTCCGCA 42

RESULT 9
AUI07928
LOCUS       AUI07928 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION ZR62348, mRNA sequence.
ACCESSION  AUI07928

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VERSION	AU107928.1	GI:13557450
KEYWORDS	EST.	
SOURCE	Human.	
ORGANISM	Homo sapiens	
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
AUTHORS	Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki ,Y., Nakamura.Y., Suyama,A. and Sugano.S.	
TITLE	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites	
JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)	
MEDLINE	21270072	
COMMENT	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yszukui@ims.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).	
FEATURES	Location/Qualifiers	
source	1..50	
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	/clone="ZRV62348"	
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	/note-"Differential display comparison of untreated and dimethylfumurate treated U937 cells"	
BASE COUNT	10 a 15 c 20 g	
ORIGIN	5 t	
Query Match	61.0%; Score 12.8; DB 9; Length 50;	
Best Local Similarity	87.5%; Pred No. 5.9e+04;	
Matches	14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Qy	2 AGCAGCAGAGTCTTC A 17	
Db	27 AGCAGCAGAGTCCGCA 42	
RESULT	10	
LOCUS	AU107929	
DEFINITION	50 bp mRNA linear EST 30-AUG-2001	
ACCESSION	ZRV62402, mRNA sequence.	
VERSION	AU107929	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1 (bases 1 to 50)	
AUTHORS	Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo.K., Sakaki ,Y., Nakamura.Y., Suyama,A. and Sugano.S.	
TITLE	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites	
JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)	
MEDLINE	21270072	
COMMENT	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yszukui@ims.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).	
FEATURES	Location/Qualifiers	
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	/note-"Differential display comparison of untreated and dimethylfumurate treated U937 cells"	
BASE COUNT	10 a 15 c 20 g	
ORIGIN	5 t	
Query Match	61.0%; Score 12.8; DB 9; Length 50;	
Best Local Similarity	87.5%; Pred No. 5.9e+04;	
Matches	14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Qy	2 AGCAGCAGAGTCTTC A 17	
Db	27 AGCAGCAGAGTCCGCA 42	
RESULT	10	
LOCUS	AU107929	
DEFINITION	50 bp mRNA linear EST 30-AUG-2001	
ACCESSION	ZRV62402, mRNA sequence.	
VERSION	AU107929	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1 (bases 1 to 50)	
AUTHORS	Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo.K., Sakaki ,Y., Nakamura.Y., Suyama,A. and Sugano.S.	
TITLE	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites	
JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)	
MEDLINE	21270072	
COMMENT	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yszukui@ims.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).	
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Matches	14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Qy	2 AGCAGCAGAGTCTTC A 17	
Db	27 AGCAGCAGAGTCCGCA 42	
RESULT	10	
LOCUS	AU107929	
DEFINITION	50 bp mRNA linear EST 30-AUG-2001	
ACCESSION	ZRV62402, mRNA sequence.	
VERSION	AU107929	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1 (bases 1 to 50)	
AUTHORS	Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo.K., Sakaki ,Y., Nakamura.Y., Suyama,A. and Sugano.S.	
TITLE	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites	
JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)	
MEDLINE	21270072	
COMMENT	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yszukui@ims.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).	
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Matches	14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Qy	2 AGCAGCAGAGTCTTC A 17	
Db	27 AGCAG	

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Best Local Similarity 78.9%; Pred. No. 6.3e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  2  AGCAGCAGAGTCTTCATCA 20
    ||| ||||| ||| ||
Db   38  AGCGCAGAGTGTCTTCCA 20

RESULT 12
A1766391/c
LOCUS      A1766391      43 bp      mRNA      linear      EST 20-DEC-1999
DEFINITION wh61d04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385223 3'
            similar to SW:COX2_HUMAN P00403 CYTOCHROME C OXIDASE POLYPEPTIDE II
            ; mRNA sequence.
ACCESSION  A1766391
VERSION     A1766391.1  GI:5232900
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 43)
AUTHORS     Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
TITLE       The WashU-HMNI Mouse EST Project
JOURNAL     Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HMNI Mouse EST Project
            Washington University School of Medicine#P
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:555512
            Trace considered overall poor quality
            possible reversed clone: similarity on wrong strand
            Seq primer: -28m13 rev1 Et from Amersham
            High quality sequence stop: 1.
FEATURES     source
            1. .43
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                /clone="IMAGE:2385223"
                /clone.lib="NCI_CGAP_Kid11"
                /lab_host="DH10B"
                /note="Organ: kidney; Vector: pT7T3D-pac (Pharmacia) with
                a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
                prepared, and ss circles were made in vitro. Following HAP
                purification, this DNA was used as tracer in a subtractive
                hybridization reaction. The driver was PCR-amplified cDNAs
                from a pool of 5,000 clones made from the same library
                (cloneIDs 1323376-1323911, 1456007-1456775, and
                1500552-1502855). Subtraction by Bento Soares and M.
                Fatima Bonaldo."
            10 a 5 c 21 g 7 t

Query Match      60.0%; Score 12.6; DB 9; Length 43;
Best Local Similarity 78.9%; Pred. No. 6.7e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  1  CAGCAGCAGAGTCTTCATC 19
    ||| ||| ||| |||||
Db   32  CATCATCATAGCTTCATC 14

RESULT 13
AA561123/c
LOCUS      AA561123      46 bp      mRNA      linear      EST 18-AUG-1997
DEFINITION v141c01.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
            IMAGE:974784 5' similar to TR:G972037 G972037 SUCCINATE
            DEHYDROGENASE ;, mRNA sequence.
ACCESSION  AA561123
VERSION     AA561123.1  GI:2332588
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1  (bases 1 to 46)
AUTHORS     Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
TITLE       The WashU-HMNI Mouse EST Project
JOURNAL     Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HMNI Mouse EST Project
            Washington University School of Medicine#P
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:555512
            Trace considered overall poor quality
            possible reversed clone: similarity on wrong strand
            Seq primer: -28m13 rev1 Et from Amersham
            High quality sequence stop: 1.
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                /dev_stage="11 weeks old"
                /lab_host="SOLR (kanamycin resistant)"
                /note="Organ: skin; Vector: pBluescript SK-; Site_1: EcoRI
                ; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo
                dt. Whole skin from 11 week old C57BL/6 female mice.
                Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
                adaptor sequence: 5' GAATTCGCACGAG 3' -3' adaptor
                sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"
            11 a 11 c 15 g 9 t

Query Match      60.0%; Score 12.6; DB 9; Length 46;
Best Local Similarity 78.9%; Pred. No. 6.9e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  1  CAGCAGCAGAGTCTTCATC 19
    ||||| ||||| ||| ||
Db   46  CAGCATCATGATTCGACG 28

RESULT 14
AUI05963/c
LOCUS      AUI05963      50 bp      mRNA      linear      EST 30-AUG-2001
DEFINITION AUI05963 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            COLF6356, mRNA sequence.
ACCESSION  AUI05963
VERSION     AUI05963.1  GI:13555484
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source

1..50
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="COLF6356"
/clone_lib="Sugano Homo sapiens cDNA library"
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BASE COUNT 11 a 14 c 13 g 12 t
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Best Local Similarity 78.9%; Pred. No. 7.2e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AGCAGCAGAGTCTTCATCA 20
||||||| | | | |
Db 21 AGCAGCAGAAATGTTCTGCA 3

RESULT 15

AU105967/c 50 bp mRNA linear EST 30-AUG-2001
LOCUS AU105967 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HRC05018, mRNA sequence.
ACCESSION AU105967
VERSION AU105967.1 GI:13555488
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source

1..50
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/db_xref="taxon:9606"
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dimethylfumarate treated U937 cells"

BASE COUNT 12 a 15 c 11 g 12 t
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Best Local Similarity 78.9%; Pred. No. 7.2e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 AGCAGCAGAGTCTTCATCA 20
||||||| | | | |
Db 48 AGCAGCAGAAATGTTCTGCA 30

Search completed: April 18, 2003, 08:55:26
Job time : 1691 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 05:56:34 ; Search time 233 Seconds

(without alignments)
202.970 Million cell updates/sec

Title: PCT-US03-05305-4

Perfect score: 21

Sequence: 1 cagcagcagatcttcattcatc 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	AAA94226	Human testostosterone
2	17.8	84.8	50	AAAX24790	Interleukin-18 bin
3	16.2	77.1	32	AAAO9140	Gos-2 promoter gen
4	16.2	77.1	50	AAAI1024	Human mature inter
5	15.2	72.4	22	AAAI5291	Mouse IL-12 p40 #1
6	15.2	72.4	40	AAZ96146	Polynucleotide seq
7	14.8	70.5	21	AAA94223	Murine testosteron
8	14.8	70.5	21	AAA94224	Murine testosteron
9	14.8	70.5	27	AAH40683	SNP specific SNPE

c 10	14.8	70.5	30	20	AAZ12445	PCR primer used to
c 11	14.8	70.5	31	15	AAQ69972	5' sense leader ex
c 12	14.6	69.5	24	24	ABL61345	Naja naja atra sho
c 13	14.6	69.5	33	24	ABK49118	Human transcrip
c 14	14.6	69.5	34	22	AAH79384	Plasmolemma regula
c 15	14.6	69.5	44	20	AAH06964	Bacillus lichenifo
c 16	14.2	67.6	20	20	AAZ31857	PCR primer for hum
c 17	14.2	67.6	20	24	ABK69555	Rat phosphorylase
c 18	14.2	67.6	22	21	AAK58494	Human PRO1283 (UNQ
c 19	14.2	67.6	22	21	AAA37208	Human PRO1283 forw
c 20	14.2	67.6	22	22	AAF54314	Primer #40 used in
c 21	14.2	67.6	24	20	AAH08676	Oligonucleotide de
c 22	14.2	67.6	24	20	AAH73404	Grand fir monoterp
c 23	14.2	67.6	26	21	AAK58495	Human PRO1283 (UNQ
c 24	14.2	67.6	26	21	AAA37209	Human PRO1283 forw
c 25	14.2	67.6	26	22	AAF54315	Primer #41 used in
c 26	14.2	67.6	30	20	AAH19511	Human lipocalin ho
c 27	14.2	67.6	34	18	AAH86354	Lambda primer 3.
c 28	13.8	65.7	18	21	AAZ57675	Human G-alpha-12 a
c 29	13.8	65.7	28	24	ABK14351	Human interleukin-
c 30	13.8	65.7	30	22	AAF28287	Oligonucleotide 5'
c 31	13.8	65.7	31	14	AAQ47780	PCR primer Lam B8
c 32	13.8	65.7	36	22	AAF56649	Human interleukin-
c 33	13.8	65.7	36	22	AAF56654	Human interleukin-
c 34	13.8	65.7	36	22	AAF56656	IL-11-IgG1-Fc dire
c 35	13.8	65.7	36	22	AAF56658	IL-11-IgG4-Fc dire
c 36	13.8	65.7	41	22	AAF28289	Modified gcc donor
c 37	13.8	65.7	50	22	AAK43508	Corneodesmosin sin
c 38	13.6	64.8	20	20	AAK95224	PCR primer used to
c 39	13.6	64.8	20	22	AAK95224	Human PARP-1 anti
c 40	13.6	64.8	23	21	AAK89796	3' RT-PCR primer u
c 41	13.6	64.8	24	24	ABK10729	SV40 RT-PCR primer
c 42	13.6	64.8	27	14	AAO40995	Annealing oligonuc
c 43	13.6	64.8	32	20	AAK25040	Cyclin-dependent k
c 44	13.6	64.8	39	16	AAK80249	Chimeric rat/human
c 45	13.6	64.8	40	17	AAH70687	Fibrin clot bindin

ALIGNMENTS

RESULT 1	AAA94226	standard; DNA; 21 BP.
ID	AAA94226	
XX	AAA94226;	
AC	AAA94226;	
DT	12-JAN-2001	(first entry)
XX	Human testostosterone-repressed prostate message-2	antisense oligo #2.
DE	Human; testostosterone-repressed prostate message-2; TRPM-2; clusterin;	
XX	sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.	
KW	Human; testostosterone-repressed prostate message-2; TRPM-2; clusterin;	
XX	sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.	
OS	Homo sapiens.	
XX	WO200049937-A2.	
PN	31-AUG-2000.	
XX	25-FEB-2000; 2000WO-US04875.	
PF	26-FEB-1999; 99US-0121726.	
XX	(UYBR-) UNIV BRITISH COLUMBIA.	
PA	Gleave M, Rennie PS, Miyake H, Nelson C;	
XX	WPI; 2000-53132/48.	
DR	Treating prostatic tumors and renal cancers by antisense inhibition of	
XX	the testostosterone-repressed prostate messenger-2 gene -	

PS Claim 3; Page 36; 38pp; English.

XX The present sequence is an antisense oligonucleotide directed at the

CC human testosterone-repressed prostate message-2 (TRPM-2, also known as

CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to

CC promote the regression of tumours, and oligonucleotides directed

CC at human TRPM-2 can be used in the treatment of tumour cells expressing

CC the TRPM-2 gene. These include prostate cancer, renal cell cancer and

CC some breast cancer cells. In addition to this, they also increase the

CC chemosensitivity of the cells, meaning that conventional chemotherapy is

CC more effective.

XX Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 Other;

Query Match 100.0%; Score 21; DB 21; Length 21;

Best Local Similarity 100.0%; Pred. No. 3.2;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGCTTCATCAT 21

DB 1 CAGCAGCAGAGCTTCATCAT 21

RESULT 2

AAAX24790/c

ID AAAX24790 standard; DNA; 50 BP.

XX

AC AAAX24790;

XX

DT 21-JUN-1999 (first entry)

XX

DE Interleukin-18 binding protein splice variant IL-18Bpa PCR primer.

XX

KW Interleukin-18 binding protein; IL-18BP; IL-18Bpa; splice variant;

KW human; autoimmune disease; inflammation; diabetes; pancreatitis;

KW rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis;

KW psoriasis; inflammatory bowel disease; multiple sclerosis;

KW ischemic heart disease; ischemic brain injury; gene therapy; PCR;

KW primer; ss.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9909063-A1.

XX

PD 25-FEB-1999.

XX

PF 13-AUG-1998; 98WO-IL00379.

XX

PR 22-JUL-1998; 98IL-0125463.

PR 14-AUG-1997; 97IL-0121554.

PR 27-AUG-1997; 97IL-0121639.

PR 29-SEP-1997; 97IL-0121860.

PR 06-NOV-1997; 97IL-0122134.

XX

PA (YEDA) YEDA RES & DEV CO LTD.

XX

PI Dinarello C, Kim SH, Novick D, Rubinstein M;

XX

DR WPI; 1999-180975/15.

XX

PT New interleukin-18 binding protein - useful for treating human

PT diseases, including autoimmune disease and inflammation

XX

PS Example 7; Page 39; 100pp; English.

XX

CC The present sequence is a reverse primer that was used with a

CC forward primer (see AAX24754) in the PCR amplification of the coding

CC region of a cDNA clone (see AAX24749) coding for human interleukin-18

CC binding protein splice variant IL-18Bpa (see AAW98004). The PCR

CC products were cut with XbaI and cloned into the XbaI site of the

CC pEF-BOS expression vector. IL-Bp18a was expressed in transfected

CC COS7 cells. The invention provides IL-18BP polypeptides capable of

CC binding IL-18 and/or modulating and/or blocking IL-18 activity.

CC These can be used to treat conditions requiring the protein

CC (claimed), such as autoimmune diseases, type 1 diabetes, rheumatoid

CC arthritis, graft rejections, inflammatory bowel disease, sepsis,

CC multiple sclerosis, ischemic heart diseases, ischemic brain injury,

CC chronic hepatitis, psoriasis, and chronic/acute pancreatitis.

XX

SQ Sequence 50 BP; 13 A; 8 C; 13 G; 16 T; 0 Other;

Query Match 84.8%; Score 17.8; DB 20; Length 50;

Best Local Similarity 90.5%; Pred. No. 99;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGCTTCATCAT 21

DB 42 CAGCAGCAGAGCTTCATCAT 22

RESULT 3

AAA09140

ID AAA09140 standard; DNA; 32 BP.

XX

AC AAA09140;

XX

DT 10-AUG-2000 (first entry)

XX

DE Gos-2 promoter gene-specific primer 1.

XX

KW maize; promoter; actin-2; enolase; Gos-2; L41; gene expression;

KW regulation; plant transformation; primer; ss.

XX

OS Zea mays.

XX

PN WO200020571-A2.

XX

PD 13-APR-2000.

XX

PF 05-OCT-1999; 99WO-US23081.

XX

PR 06-OCT-1998; 98US-0103294.

PR 05-NOV-1998; 98US-0107201.

XX

PA (PION-) PIONEER HI-BRED INT INC.

PA (AGER-) AGERI AGRIC GENETIC ENG RES INST.

XX

PI Barbour E, Meyer TE, Saad ME;

XX

DR WPI; 2000-303763/26.

XX

PT Novel maize promoters used for producing transgenic plants with

PT regulated expression of heterologous nucleotide sequences

XX

PS Example 1; Page 26; 48pp; English.

XX

CC Novel maize promoters (AAA09134-37) that drive expression of actin-2,

CC enolase, Gos-2 or L41, respectively, were isolated from genomic DNA

CC using PCR. The first round of PCR was performed on each DNA sample

CC using PCR. The first round of PCR was performed on each DNA sample with

CC Clontech primer AP1 (AAA09138) and a gene-specific primer 1

CC (AAA09139-42), in a second round of PCR using Clontech primer AP2

CC (AAA09143) and a gene-specific primer 2 (AAA09144-47). Clones were

CC sequenced for verification and then amplified with Clontech primer AP3

CC (AAA09148) and a gene-specific primer (AAA09149-52). The promoters are

CC used for regulating the expression of heterologous nucleotide sequences

CC to vary the phenotype of a plant, e.g. modifying fatty acid composition,

CC altering amino acid content and altering the pathogen defense system of

CC the plant. Plants comprising important commercial traits can be

CC generated.

XX

SQ Sequence 32 BP; 8 A; 12 C; 6 G; 6 T; 0 Other;

Query Match 77.1%; Score 16.2; DB 21; Length 32;

Best Local Similarity 85.7%; Pred. No. 4.9e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGCTCTTCATCAT 21
 ||||| ||||| ||||| ||||| |||||

Db 3 CAGCAGCAGAGCTCTTCATCAT 23

RESULT 4
 AAA11024/c
 ID AAA11024 standard; DNA; 50 BP.

XX AC AA11024;
 XX 28-JUL-2000 (first entry)

DE Human mature interleukin 18 binding protein coding sequence primer #2.
 XX
 XX
 KW Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
 KW regulator; drug; sensitivity disease; organ rejection; organ transplant;
 KW autoimmune disease; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX WO200012555-A1.
 PN 09-MAR-2000.
 PD 18-NOV-1998; 98WO-JP05186.
 XX 01-SEP-1998; 98JP-0247588.
 PR 18-NOV-1998; 98JP-0327914.
 XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 PA Torigoe K, Taniat M, Kurimoto M;
 PI WPI; 2000-237850/20.
 DR Interleukin 18-binding protein with activity of regulating
 PT physiological actions of interleukin 18, useful as regulator and drug
 PT for sensitivity diseases and organ rejection and in treating diseases
 PT due to excess immune reaction -
 XX Example 2; Page 22; 71pp; Japanese.
 XX The invention relates to novel interleukin 18 (IL-18)-binding proteins
 CC from humans or mice which act as regulators and drugs for sensitivity
 CC diseases and organ rejection and in treating diseases due to excess
 CC immune reaction, e.g. in slowing down rejection after organ transplant,
 CC and in treating autoimmune diseases. This sequence represents a PCR
 CC primer used to isolate the coding sequence for the human mature
 CC interleukin 12 binding protein (AA11002).

XX Sequence 50 BP; 7 A; 11 C; 18 G; 14 T; 0 other;

Query Match 77.1%; Score 16.2; DB 21; Length 50;
 Best Local Similarity 85.7%; Pred. No. 5.2e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGCTCTTCATCAT 21
 ||||| ||||| ||||| ||||| |||||

Db 44 CAGCAGCAGAGCTCTTCATCAT 24

RESULT 5
 AAS15291
 ID AAS15291 standard; DNA; 22 BP.
 XX AAS15291;
 AC 16-JAN-2002 (first entry)
 XX
 DT Mouse IL-12 p40 #1 PCR primer 662F.
 DE

XX Mouse; ss; PCR primer; neurotropic; neuroprotective; 662F;
 KW antiinflammatory; interleukin-lbeta; IL-1b; tumour necrosis factoralpha;
 KW TNFalpha; macrophage inflammatory protein-lalpha; MIP-lalpha;
 KW fractalkane; glial fibrillar associated protein; GFAP; MHC; CX3CR1; CD86;
 KW major histocompatibility complex; Alzheimer's disease; cerebral ischaemia;
 KW neurodegenerative disease; VitD3-24OHase; MCP-1; IL-10; IL-12 p40;
 KW IFN-gamma; CD3 epsilon; CD4; IgG-1; Ig k; osteopontin.
 XX
 OS Mus sp.
 XX WO200175165-A2.
 PN 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US10247.
 PF 30-MAR-2000; 2000US-193847P.
 PR (ELAN-) ELAN PHARM INC.
 XX McConlogue LC, Games KD, Yednock TA, Hua T, Messersmith E, Bard F;
 PI WPI; 2001-639367/73.
 XX Selecting compounds useful for treating or preventing Alzheimer's
 PT disease, from their ability to reduce levels of specific disease
 PT markers in animal models -
 XX Example 5; Page 23; 36pp; English.
 XX The invention relates selecting compounds that reduce symptoms of
 CC Alzheimer's disease using a non-human mammal that has been subjected to
 CC cerebral ischaemia or lesion of a nerve so as to produce, in the
 CC affected region, increased levels of specific markers of Alzheimer's
 CC disease-associated inflammation. Test compounds are selected if they
 CC reduce levels of these markers significantly, in the affected region,
 CC relative to controls. The markers are interleukin-lbeta (IL-1b), tumour
 CC necrosis factoralpha (TNFalpha), macrophage inflammatory protein-lalpha
 CC (MIP-lalpha), glial fibrillar associated protein (GFAP), MHC (major
 CC histocompatibility complex) Iialpha or II L, CD86, fractalkane or CX3CR1
 CC (a receptor for fractalkane). The method is used to identify compounds
 CC useful in treatment or prevention of Alzheimer's disease or other
 CC neurodegenerative diseases that have an inflammatory component. The
 CC method provides fast, accurate and quantitative drug screens.
 CC The present sequence is a PCR primer used to determine the level of
 CC a transcript for an efficacy marker in a transgenic mouse which
 CC overexpresses App and displays Alzheimer's like neuropathology. The
 CC efficacy markers are VitD3-24OHase, MCP-1, IL-10, IL-12 p40, #1/#2,
 CC IFN-gamma #1/#2, CD3 epsilon, CD4 #1/#2, IgG-1, Ig k (light chain).

XX Sequence 22 BP; 6 A; 8 C; 3 G; 5 T; 0 other;

Query Match 72.4%; Score 15.2; DB 22; Length 22;
 Best Local Similarity 85.0%; Pred. No. 1.3e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGCTCTTCATCA 20
 ||||| ||||| ||||| ||||| |||||

Db 2 CAGCAGCAGAGCTCTTCATCA 21

RESULT 6
 AA296146/c
 ID AA296146 standard; DNA; 40 BP.
 XX AA296146;
 AC 10-APR-2000 (first entry)
 XX Polynucleotide sequence including binding site for BamHI.
 DE Ligand binding; restriction enzyme; nucleic acid determination;
 KW

```

KW pharmaceutical; BamHI; ss.
XX Synthetic.
OS WO9963077-A2.
PN 09-DEC-1999.
XX 04-JUN-1999; 99WO-US12516.
XX 04-JUN-1998; 98US-0087905.
PR 03-JUN-1999; 99US-0324672.
XX (TWTE-) TM TECHNOLOGIES INC.
PA Lane MJ, Benight AS, Faldasz BD;
PI WPI; 2000-116369/10.
XX Modulating polynucleotide ligand binding site affinity using
XX determination of the flanking duplex sequences -
XX Example 1; Page 45; 62pp; English.
XX The invention provides a method for determining the sequence of
XX polynucleotide flanking regions that modulate ligand binding
XX characteristics of an adjacent binding site. The method comprises:
XX (i) providing a number of different duplex polynucleotides, each having
XX the same polynucleotide ligand binding site and a randomly synthesised
XX sequence flanking the binding site; (ii) exposing the duplex to a ligand
XX selective for the binding site; (iii) isolating the duplexes which bind or
XX do not bind the ligand; and (iv) determining the nucleotide composition
XX of the flanking duplex sequence by sequencing the duplex sequence
XX adjacent to the binding site. The invention is used to modulate the
XX ligand-binding characteristics of any nucleotide sequence. The invention
XX is less costly and more efficient than prior art techniques that moderate
XX ligand binding using small molecule pharmaceuticals. Sequences
XX AA295762-236170 represent polynucleotide sequences including the binding
XX site for the restriction enzyme BamHI and used in the course of the
XX invention.
XX Sequence 40 BP; 6 A; 5 C; 19 G; 10 T; 0 other;
XX
XX Query Match 72.4%; Score 15.2; DB 21; Length 40;
XX Best Local Similarity 85.0%; Pred. No. 1.4e+03;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1 CAGCAGCAGAGTCTTCATCA 20
Db 28 CAGCAACAGGCTTCTCA 9
XX
RESULT 7
AAA94223
ID AAA94223 standard; DNA; 21 BP.
XX
AC AAA94223;
XX
XX 12-JAN-2001 (first entry)
XX
DE Murine testosterone-repressed prostate message-2 antisense oligo #1.
XX
XX Mouse; testosterone-repressed prostate message-2; TRPM-2; clusterin;
KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /*mod_base= OTHER
FT /*note= "phosphorothioate backbone"
XX
PN WO200049937-A2.
XX 31-AUG-2000.
XX 25-FEB-2000; 2000WO-US04875.
XX 26-FEB-1999; 99US-0121726.
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX Gleave M, Rennie PS, Miyake H, Nelson C;
XX WPI; 2000-533132/48.
XX Treating prostatic tumors and renal cancers by antisense inhibition of
XX the testosterone-repressed prostate messenger-2 gene -
XX Example 1; Page 35; 38pp; English.
XX The present sequence is an antisense oligonucleotide directed at the
XX murine testosterone-repressed prostate message-2 (TRPM-2), also known as
XX clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to
XX promote the regression of tumours in mice, and oligonucleotides directed
XX at human TRPM-2 can be used in the treatment of tumour cells expressing
XX the TRPM-2 gene. These include prostate cancer, renal cell cancer and
XX some breast cancer cells. In addition to this, they also increase the
XX chemosensitivity of the cells, meaning that conventional chemotherapy is
XX more effective.
XX Sequence 21 BP; 7 A; 5 C; 5 G; 4 T; 0 other;
XX
XX Query Match 70.5%; Score 14.8; DB 21; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 2e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 CAGCAGCAGAGTCTTCAT 18
Db 4 CAGCAGGAGAAATCTTCAT 21
XX
RESULT 8
AAA94224
ID AAA94224 standard; DNA; 21 BP.
XX
AC AAA94224;
XX
XX 12-JAN-2001 (first entry)
XX
DE Murine testosterone-repressed prostate message-2 antisense control.
XX
XX Mouse; testosterone-repressed prostate message-2; TRPM-2; clusterin;
KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
XX
OS Mus sp.
XX
PN WO200049937-A2.
XX 31-AUG-2000.
XX 25-FEB-2000; 2000WO-US04875.
XX 26-FEB-1999; 99US-0121726.
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX Gleave M, Rennie PS, Miyake H, Nelson C;
XX WPI; 2000-533132/48.
XX Treating prostatic tumors and renal cancers by antisense inhibition of
XX the testosterone-repressed prostate messenger-2 gene -
XX Example 1; Page 35; 38pp; English.
XX

```

XX CC The present sequence is a mismatch control used with an antisense
CC oligonucleotide directed at the murine testosterone-repressed prostate
CC message-2 (TRPM-2, also known as clusterin, sulfated glycoprotein-2 or
CC SGP-2). The antisense sequence was shown to promote the regression of
CC tumours in mice, and similar oligonucleotides directed at human TRPM-2
CC can be used in the treatment of tumour cells expressing the TRPM-2 gene.
CC These include prostate cancer, renal cell cancer and some breast cancer
CC cells. In addition to this, they also increase the chemosensitivity of
CC the cells, meaning that conventional chemotherapy is more effective.
XX SQ Sequence 21 BP; 6 A; 6 C; 5 G; 4 T; 0 other;
Query Match 70.5%; Score 14.8; DB 21; Length 21;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CAGCAGCAGAGTCTTCAT 18
||||||| |||||
Db 4 CAGCAGCAGAGTCTTCAT 21
RESULT 9
AAH40683/C
ID AAH40683 standard; DNA; 27 BP.
XX AC AAH40683;
XX DT 14-AUG-2001 (first entry)
XX DE SNP specific SNPE primer SEQ ID 3479.
XX KW Single nucleotide polymorphism: SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia, diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; primer; ss.
XX OS Homo sapiens.
XX PN WO200129262-A2.
XX PD 26-APR-2001.
XX PF 13-OCT-2000; 2000WO-US28436.
XX PR 15-OCT-1999; 99US-0160096.
XX PA (ORCH-) ORCHID BIOSCIENCES INC.
XX PI Picoult-Newburg L, Pohl M;
XX DR WPI; 2001-290930/30.
XX PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample
XX PS Claim 1; Page 67; 83pp; English.
XX CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a single nucleotide
CC primer extension (SNPE) primer specific for a human SNP containing DNA
CC sequence.
XX SQ Sequence 27 BP; 5 A; 8 C; 4 G; 9 T; 1 other;
Query Match 70.5%; Score 14.8; DB 22; Length 27;
Best Local Similarity 84.2%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 AGCAGCAGAGTCTTCATCA 20
||||||| || |||||
Db 22 AGCAGCAGAGTCTTCATCA 4
RESULT 10
AAZ12445/C
ID AAZ12445 standard; DNA; 30 BP.
XX AC AAZ12445;
XX DT 08-OCT-1999 (first entry)
XX DE PCR primer used to amplify ORF83 of Neisseria species.
XX KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW treatment; Neisseria infection; meningitis; septicaemia; gonorrhea;
KW PCR primer; ss.
XX OS Synthetic.
XX OS Neisseria sp.
XX PN WO9924578-A2.
XX PD 20-MAY-1999.
XX PF 09-OCT-1998; 98WO-IB01665.
XX PR 01-SEP-1998; 98GB-0019016.
XX PR 06-NOV-1997; 97GB-0023516.
XX PR 14-NOV-1997; 97GB-0024190.
XX PR 18-NOV-1997; 97GB-0024386.
XX PR 27-NOV-1997; 97GB-0025158.
XX PR 10-DEC-1997; 97GB-0026147.
XX PR 14-JAN-1998; 98GB-0000759.
XX PA (CHIR-) CHIRON SPA.
XX PI Grandi G, Massignani V, Pizza M, Rappuoli R, Scarlato V;
XX DR WPI; 1999-327407/27.
XX PT Proteins from Neisseria meningitidis and N. gonorrhoeae useful for
XX diagnosis, treatment and prevention of infection
XX PS Disclosure; Page 489; 524pp; English.
XX CC PCR primers AAZ12359-Z12531 were used to amplify various open reading
CC frames (ORFs) of Neisseria meningitidis and N. gonorrhoeae. These
CC ORFs (AAZ11972-Z12358) encode antigenic proteins (AAZ38499-Y38944). The
CC antigenic proteins, their fragments, their nucleic acids and antibodies
CC are used for diagnosis, prevention (as vaccines) or treatment of
CC Neisseria infections, such as meningitis, septicaemia and gonorrhea.
CC Both organisms are closely related. Fragments of the nucleic acids are

```
CC useful as hybridisation probes and antisense reagents.
XX
SQ Sequence 30 BP; 7 A; 10 C; 7 G; 6 T; 0 other;

Query Match 70.5%; Score 14.8; DB 20; Length 30;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCAT 18
Db 29 CAGCAGCAGGTTTCAT 12
||||| || |||||

RESULT 11
AAQ69972/c
ID AAQ69972 standard; cDNA; 31 BP.
XX
AC AAQ69972;
XX
XX 13-MAR-1995 (first entry)
XX
XX 5'sense leader ex oligo primer to amplify 5' end Can fi cDNA.
XX
XX Canis familiaris; protein allergen; dog dander; dog hair; allergy;
XX T cell response; stimulation; diagnosis; sensitivity; therapeutic;
XX agents; PCR; polymerase chain reaction; primer; amplification;
XX probe; hybridisation; partial cDNA; degenerate; ss.
XX
XX Synthetic.
XX
XX WO9416068-A.
XX
XX 21-JUL-1994.
XX
XX 30-DEC-1993; 93WO-US12468.
XX
XX 31-DEC-1992; 92US-0999712.
XX 22-NOV-1993; 93US-0156549.
XX
XX (IMMU-) IMMULOGIC PHARM CORP.
XX
XX Bizinkauskas CB, Brauer AW, Konieczny A, Morgenstern JP;
XX
XX WPI; 1994-249215/30.
XX
XX DNA encoding dog dander allergenic peptide(s) Can f I and Can f
XX II - used in the diagnosis and treatment of sensitivity to dog
XX dander
XX
XX Example 2; Page 59; 124pp; English.
XX
XX AAQ69972 is a 5' primer corresponding to residues -26 to -20 of Canfi
XX (AAR59987). It is used with AAQ69973 to amplify and sequence the 5' end
XX of the Can fi cDNA. Peptides of the invention have the ability to
XX induce a T cell response, which may include T cell stimulation or
XX T cell nonresponsiveness. Some have the ability to bind the dog
XX dander specific IgE of dog dander allergic subjects. These peptides
XX are useful in diagnosing sensitivity to dog dander. Other peptides
XX significantly reduce the ability to bind dog dander allergic IgE and
XX are thus useful as therapeutic agents. (See also AAQ69951-Q70006 and
XX AAR59987-60018 - these include primers, and probes for isolation of
XX cDNA coding Can fi and fII allergens and peptides derived from the
XX sequences.)
XX
XX Sequence 31 BP; 7 A; 13 C; 5 G; 6 T; 0 other;

Query Match 70.5%; Score 14.8; DB 15; Length 31;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCAGCAGAGTCTTCATC 19
Db 24 AGGAGCAGGCTCTTCATC 7
||||| ||||| |||||
```

```
RESULT 12
ABL61345/c
ID ABL61345 standard; DNA; 24 BP.
XX
XX ABL61345;
AC ABL61345;
XX
XX 13-SEP-2002 (first entry)
DT
XX
XX Naja naja atra short chain neurotoxin-associated PCR primer #1.
DE
XX
XX Chinese cobra; neurotoxin; cancer; PCR; primer; ss.
KW
XX
XX Naja naja atra.
OS
XX
XX CN1337404-A.
XX
XX 27-FEB-2002.
XX
XX 03-AUG-2000; 2000CN-0119561.
XX
XX 03-AUG-2000; 2000CN-0119561.
PR
XX (SHAN-) SHANGHAI BIOENGINEERING RES CENT CHINESE.
XX
XX Cai Q, Yang S, Gong Y;
PI
XX
XX WPI; 2002-384228/42.
XX
XX Short-chain nervous cobra toxin, its preparation and use -
XX Example 1; Page 11; 30pp; Chinese.
XX
XX This invention describes a novel cobra short chain neurotoxin, the
XX polynucleotide encoding the polypeptide and the method for producing the
XX polypeptide by means of recombination technology. The invention also
XX discloses the method for curing several diseases, such as cancer, by
XX using the cobra short chain neurotoxin, and a medicine composite
XX containing the cobra short chain neurotoxin. This sequence represents a
XX PCR primer used in the amplification of the short chain neurotoxin
XX described in the method of the invention.
XX
XX Sequence 24 BP; 7 A; 5 C; 6 G; 6 T; 0 other;

Query Match 69.5%; Score 14.6; DB 24; Length 24;
Best Local Similarity 81.0%; Pred. No. 2.5e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
Db 21 CAGCAACAGAGTTTCCATCTT 1
||||| ||||| ||||| |||||

RESULT 13
ABK49118/c
ID ABR49118 standard; DNA; 33 BP.
XX
AC ABK49118;
XX
XX 02-JUL-2002 (first entry)
DT
XX
XX Human transcription factor LCR-FI9.02 PCR primer #1.
DE
XX
XX Human; ss; transcription factor; LCR-FI9.02; erythropathy; PCR; primer.
XX
XX Homo sapiens.
OS
XX
XX WO200220583-A1.
XX
XX 14-MAR-2002.
XX
XX 25-JUN-2001; 2001WO-CN01053.
XX
XX
```

XX PR 28-JUN-2000; 2000CN-0116922.
XX PA (SHAN-) SHANGHAI BLOWNDOW GENE DEV INC.
XX PT Mao Y, Xie X;
XX DR WPI; 2002-351761/38.
XX XX Homo transcription factor F19.02 and encoding polynucleotide, used in
XX PT treatment of erythropathy -
XX PS Example 4; Page 18; 38pp; Chinese.
XX XX The invention relates to an isolated polypeptide of human (HOMO)
XX CC transcription factor ICR-F19.02 the cDNA encoding it, and its fragment,
XX CC analogue or derivative. Also included are vectors expressing the protein,
XX CC a host cell comprising the vector, the isolation of modulators of the
XX CC protein and an anti-transcription factor ICR-F19.02 antibody. The protein
XX CC and nucleic acid are used in diagnosis and treatment of erythropathy.
XX CC The present sequence is a PCR primer used to clone the cDNA encoding
XX CC transcription factor ICR-F19.02.
XX SQ Sequence 33 BP; 7 A; 9 C; 8 G; 9 T; 0 other;
Query Match 69.5%; Score 14.6; DB 24; Length 33;
Best Local Similarity 81.0%; Pred. No. 2.6e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CAGCAGCAGAGCTCTTCATCAT 21
DB 27 CAGCAGCAGCAGCTGTCATCAT 7
RESULT 14
ID AAH79384/C
XX AAH79384 standard; DNA; 34 BP.
XX AC AAH79384;
XX DT 04-DEC-2001 (first entry)
XX DE Plasmolemma regulation function-contained protein 70 CDNA PCR primer #3.
XX KW Plasmolemma regulation function-contained protein 70; cancer; HIV;
XX XX infection; gene therapy; human; PCR primer; ss.
XX OS Homo sapiens.
XX CN1302889-A.
XX PN 11-JUL-2001.
XX PD 29-OCT-1999; 99CN-0119927.
XX PF 29-OCT-1999; 99CN-0119927.
XX PR 29-OCT-1999; 99CN-0119927.
XX XX (BODA-) BODAO GENE TECHNOLOGY CO LTD SHANGHAI.
XX PI Mao Y, Xie Y;
XX WPI; 2001-566050/64.
XX DR Polypeptide-human protein 70 containing plasmolemma regulation function
XX PT and polynucleotide for coding it -
XX PS Example 5; Page 15(Disclosure); 27pp; Chinese.
XX CC The present invention provides the protein and coding sequences of human
XX CC plasmolemma regulation function-contained protein 70. The sequences can
XX CC be used in the treatment of cancer and HIV infection. The present
XX CC sequence is a PCR primer for the coding sequence of the invention.

SQ Sequence 34 BP; 5 A; 9 C; 9 G; 11 T; 0 other;
Query Match 69.5%; Score 14.6; DB 22; Length 34;
Best Local Similarity 81.0%; Pred. No. 2.6e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CAGCAGCAGAGCTCTTCATCAT 21
DB 27 CAACAGAGAGCGCTTCATCAT 7
RESULT 15
ID AAX06964 standard; DNA; 44 BP.
XX AAX06964;
XX AC AAX06964;
XX DT 10-MAY-1999 (first entry)
XX DE Bacillus licheniformis xyloglucanase primer Xyloglu.upper.PstI.
XX KW Xyloglucanase; detergent; PCR; primer; ss.
XX OS Synthetic.
XX OS Bacillus licheniformis.
XX PN WO9902663-A1.
XX PD 21-JAN-1999.
XX PF 01-JUL-1998; 98WO-DK00290.
XX PR 24-OCT-1997; 97DK-0001213.
XX PR 07-JUL-1997; 97DK-0000822.
XX PA (NOVO) NOVO-NORDISK AS.
XX PI Bjornvad ME, Jorgensen PL, Outtrup H, Schuelein M;
XX DR WPI; 1999-120866/10.
XX XX New enzyme preparation comprising a xyloglucanase with an activity
XX PT of 50 % at pH 7 - useful for improving the properties of cellulosic
XX PT fibres, yarn, (non)woven fabric, and ratting hemp, jute, flax and
XX PT linen fibres
XX PS Example 5; Page 60; 87pp; English.
XX CC Primers Xyloglu.upper.PstI and Xyloglu.lower.NotI (see AAX06965) were
XX CC used for the PCR amplification of Bacillus licheniformis ATCC 14580
XX CC xyloglucosidase DNA (see also AAX06949), using chromosomal DNA as
XX CC template. The primers incorporate PstI and NotI sites into the
XX CC amplified DNA. The PCR product was ligated into plasmid pMO1944, a
XX CC pUB110 derivative containing elements making it propagatable in
XX CC Bacillus subtilis. The B. licheniformis xyloglucanase (see AAX06962)
XX CC was expressed in transformed B. subtilis PL2954 cells. The enzyme
XX CC is useful for improving the properties of cellulosic fabrics and in
XX CC detergent compositions.
XX SQ Sequence 44 BP; 7 A; 16 C; 12 G; 9 T; 0 other;
Query Match 69.5%; Score 14.6; DB 20; Length 44;
Best Local Similarity 81.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CAGCAGCAGAGCTCTTCATCAT 21
DB 12 CAGCAGCGCGGCTTCGTCAT 32
Search completed: April 18, 2003, 07:51:31
Job time : 239 secs

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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 07:47:42 ; Search time 52 Seconds
(without-alignments)
123.850 Million cell updates/sec

Title: PCT-US03-05305-4

Perfect score: 21

Sequence: 1 cagcagcagagtttcattcat 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.4	73.3	45	1	US-07-885-689A-7
2	14.8	70.5	31	2	US-08-467-603-35
3	14.8	70.5	31	2	US-08-466-793-35
4	14.8	70.5	31	2	US-08-491-861A-35
5	14.6	69.5	44	4	US-09-110-959A-11
6	14.2	67.6	20	2	US-09-205-860-3
7	14.2	67.6	20	4	US-09-657-452A-163
8	14.2	67.6	24	4	US-09-360-545-57
9	14.2	67.6	30	3	US-09-130-663-10
10	14.2	67.6	30	3	US-09-432-335-10
11	14.2	67.6	30	4	US-09-234-023B-20
12	14.2	67.6	30	4	US-09-614-022-10
13	13.8	65.7	18	2	US-09-256-496-15
14	13.8	65.7	37	2	US-08-467-603-54
15	13.8	65.7	37	2	US-08-466-793-54
16	13.8	65.7	37	2	US-08-491-861A-54
17	13.6	64.8	20	4	US-09-517-467B-87
18	13.6	64.8	23	4	US-09-489-085A-6
19	13.6	64.8	27	6	5463174-1
20	13.4	63.8	20	4	US-09-657-452A-162
21	13.4	63.8	34	1	US-08-373-124A-27
22	13.4	63.8	34	1	US-08-435-628-27
23	13.2	62.9	18	2	US-09-205-860-28
24	13.2	62.9	24	4	US-09-442-099A-9
25	13.2	62.9	33	2	US-08-343-443B-100
26	13.2	62.9	38	3	US-09-130-663-26
27	13.2	62.9	38	3	US-09-432-335-26

c	28	13.2	62.9	38	4	US-09-614-022-26	Sequence 26, Appl
c	29	13	61.9	23	1	US-08-390-850-363	Sequence 363, App
c	30	13	61.9	23	1	US-08-435-634-363	Sequence 363, App
c	31	13	61.9	31	1	US-08-390-850-93	Sequence 93, Appl
c	32	13	61.9	31	1	US-08-390-850-94	Sequence 94, Appl
c	33	13	61.9	31	1	US-08-390-850-95	Sequence 95, Appl
c	34	13	61.9	31	1	US-08-435-634-93	Sequence 93, Appl
c	35	13	61.9	31	1	US-08-435-634-94	Sequence 94, Appl
c	36	13	61.9	31	1	US-08-435-634-95	Sequence 95, Appl
c	37	13	61.9	34	3	US-09-082-664-2	Sequence 2, Appl
c	38	13	61.9	40	2	US-08-713-815A-6	Sequence 6, Appl
c	39	13	61.9	44	3	US-08-782-480-11	Sequence 11, Appl
c	40	13	61.9	44	4	US-08-954-211-11	Sequence 11, Appl
c	41	13	61.9	44	4	US-09-005-167A-11	Sequence 11, Appl
c	42	13	61.9	44	4	US-09-176-741B-11	Sequence 11, Appl
c	43	13	61.9	45	3	US-08-721-458B-62	Sequence 62, Appl
c	44	12.8	61.0	27	3	US-08-985-162-1581	Sequence 1581, Ap
c	45	12.8	61.0	27	4	US-08-584-040-393	Sequence 393, App

ALIGNMENTS

RESULT 1
US-07-885-689A-7
; Sequence 7, Application US/07885689A
; Patent No. 5366876
; GENERAL INFORMATION:
; APPLICANT: Cho, Joong M.
; APPLICANT: Lee, Tae H.
; APPLICANT: Chung, Hyun H.
; APPLICANT: Lee, Yong B.
; APPLICANT: Lee, Tae G.
; APPLICANT: Park, Young W.
; APPLICANT: Han, Kyu B.
; TITLE OF INVENTION: Method for Production of Bovine Growth
; HORMONE USING A SYNTHETIC GENE.
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolash & Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/885,689A
; FILING DATE: 19-MAY-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 377-144P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..45
; OTHER INFORMATION: /label= oligonucleotide

CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII-text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/491.861A
 FILING DATE: 27-OCT-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/999,712
 FILING DATE: 31-Dec-92
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragouras, Amy E.
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: IMI-026CP(IPC-048CP)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 742-4214
 INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 31 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-491-861A-35

Query Match 70.5%; Score 14.8; DB 2; Length 31;
 Best Local Similarity 88.9%; Pred. No. 3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCAGCAGAGTCTTCATC 19
 DB 24 AGGAGCAGGCTTCATC 7

RESULT 5
 US-09-110-959A-11
 Sequence 11, Application US/09110959A
 Patent No. 6268197
 GENERAL INFORMATION:
 APPLICANT: Schuelein, Martin
 APPLICANT: Outtrup, Helle
 APPLICANT: Jorgensen, Per Lina
 APPLICANT: Bjornvad, Nads Eskelund
 TITLE OF INVENTION: Alkaline xyloglucanase
 FILE REFERENCE: 5206.200-US
 CURRENT APPLICATION NUMBER: US/09/110,959A
 CURRENT FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 0822/97
 PRIOR FILING DATE: 1997-07-07
 PRIOR APPLICATION NUMBER: 1213/97
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/054,039
 PRIOR FILING DATE: 1997-07-28
 PRIOR APPLICATION NUMBER: 60/063,694
 PRIOR FILING DATE: 1997-10-28
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 11
 LENGTH: 44
 TYPE: DNA
 ORGANISM: Bacillus sp.

Query Match 69.5%; Score 14.6; DB 4; Length 44;
 Best Local Similarity 81.0%; Pred. No. 3.8e+02;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCATC 21
 DB 12 CAGCAGCGCGGCTTCGTCAT 32
 RESULT 6
 US-09-205-860-3
 Sequence 3, Application US/09205860
 Patent No. 5981732
 GENERAL INFORMATION:
 APPLICANT: Lex M. Cowsett
 TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-13 EXPRESSION
 FILE REFERENCE: RTS-0031
 CURRENT APPLICATION NUMBER: US/09/205,860
 CURRENT FILING DATE: 1998-12-04
 NUMBER OF SEQ ID NOS: 87
 SEQ ID NO 3
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: PCR Primer
 US-09-205-860-3

Query Match 67.6%; Score 14.2; DB 2; Length 20;
 Best Local Similarity 84.2%; Pred. No. 5.2e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATC 19
 DB 2 CAGCAGCAGAGTCTTCACC 20

RESULT 7
 US-09-657-452A-163
 Sequence 163, Application US/09657452A
 Patent No. 6426188
 GENERAL INFORMATION:
 APPLICANT: Brett P. Monia
 APPLICANT: Jacqueline Wyatt
 TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHORYLASE KINASE ALPHA 1 EXPRESSION
 FILE REFERENCE: RTS-0125
 CURRENT APPLICATION NUMBER: US/09/657,452A
 CURRENT FILING DATE: 2000-09-07
 NUMBER OF SEQ ID NOS: 178
 SEQ ID NO 163
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Antisense oligonucleotide
 US-09-657-452A-163

Query Match 67.6%; Score 14.2; DB 4; Length 20;
 Best Local Similarity 84.2%; Pred. No. 5.2e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATC 19
 DB 2 CATCATCATAGTCTTCATC 20

RESULT 8
 US-09-360-545-57/c
 Sequence 57, Application US/09360545
 Patent No. 6429014
 GENERAL INFORMATION:
 APPLICANT: Croteau, Rodney B
 APPLICANT: Bohlmann, Jorg
 APPLICANT: Steele, Christopher L
 APPLICANT: Phillips, Michael A
 TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)

FILE REFERENCE: wsr13885
CURRENT APPLICATION NUMBER: US/09/360,545
CURRENT FILING DATE: 1999-07-26
EARLIER APPLICATION NUMBER: 60/052,249
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: PCT/US98/14528
EARLIER FILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 57
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: oligonucleotide corresponding to amino acid
OTHER INFORMATION: sequence set forth in SEQ ID NO:46
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(24)
OTHER INFORMATION: oligonucleotide that corresponds to the conserved
OTHER INFORMATION: amino acid sequence set forth in SEQ ID NO:46
US-09-360-545-57

Query Match 67.6%; Score 14.2; DB 4; Length 24;
Best Local Similarity 84.2%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATC 19
Db 24 CAGCAGCAGAGTCTTCAC 6
|||||

RESULT 9
US-09-130-663-10/c
Sequence 10, Application US/09130663A
Patent No. 6020163
GENERAL INFORMATION:
APPLICANT: Konklin, Darrell C.
TITLE OF INVENTION: LIPOCALIN HOMOLOG
FILE REFERENCE: 97-24
CURRENT APPLICATION NUMBER: US/09/130,663A
CURRENT FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 60/054,867
EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer: ZC13270
US-09-130-663-10

Query Match 67.6%; Score 14.2; DB 3; Length 30;
Best Local Similarity 84.2%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATC 19
Db 27 CAGGACAGGGTCTTCATC 9
|||||

RESULT 10
US-09-432-335-10/c
Sequence 10, Application US/09432335
Patent No. 6143720
GENERAL INFORMATION:
APPLICANT: Konklin, Darrell C.
TITLE OF INVENTION: LIPOCALIN HOMOLOG
FILE REFERENCE: 97-24
CURRENT APPLICATION NUMBER: US/09/432,335

CURRENT FILING DATE: 1999-11-02
EARLIER APPLICATION NUMBER: 09/130,663
EARLIER FILING DATE: 1998-08-06
EARLIER APPLICATION NUMBER: 60/054,867
EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer: ZC13270
US-09-432-335-10

Query Match 67.6%; Score 14.2; DB 3; Length 30;
Best Local Similarity 84.2%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATC 19
Db 27 CAGGACAGGGTCTTCATC 9
|||||

RESULT 11
US-09-254-023B-20
Sequence 20, Application US/09254023B
Patent No. 6225077
GENERAL INFORMATION:
APPLICANT: SCHMIDT, Gunter
THOMPSON, Andrew Hugin
TITLE OF INVENTION: CHARACTERISING DNA
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis, LLP
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/254,023B
FILING DATE: 20-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB97/02403
FILING DATE: 05-SEP-1997
APPLICATION NUMBER: GB 9618544.2
FILING DATE: 05-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa Stanek
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 020600-275
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-254-023B-20

Query Match 67.6%; Score 14.2; DB 4; Length 30;
Best Local Similarity 84.2%; Pred. No. 5.5e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCAGCAGAGCTCTTCATC 21
 |||||
 Db 1 GCAGCAGAGCTCTTCATC 19

RESULT 12

US-09-614-022-10/c
 ; Sequence 10, Application US/09614022
 ; Patent No. 6365716
 ; GENERAL INFORMATION:
 ; APPLICANT: Konklin, Darrell C.
 ; TITLE OF INVENTION: LIPOCALIN HOMOLOG
 ; FILE REFERENCE: 97-24
 ; CURRENT APPLICATION NUMBER: US/09/614,022
 ; CURRENT FILING DATE: 2000-07-11
 ; PRIOR APPLICATION NUMBER: 09/130,663
 ; PRIOR FILING DATE: 1998-08-06
 ; PRIOR APPLICATION NUMBER: 60/054,867
 ; PRIOR FILING DATE: 1997-08-06
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 10
 ; LENGTH: 30
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Oligonucleotide primer: 2C13270
 US-09-614-022-10

Query Match 67.6%; Score 14.2; DB 4; Length 30;
 Best Local Similarity 84.2%; Pred. No. 5.5e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGCTCTTCATC 19
 |||||
 Db 27 CAGGACAGGCTCTTCATC 9

RESULT 13

US-09-256-496-15
 ; Sequence 15, Application US/09256496
 ; Patent No. 5998206
 ; GENERAL INFORMATION:
 ; APPLICANT: Lex M. Cowsett
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF G-APLHA-12 EXPRESSION
 ; FILE REFERENCE: RTS-0056
 ; CURRENT APPLICATION NUMBER: US/09/256,496
 ; CURRENT FILING DATE: 1999-02-23
 ; NUMBER OF SEQ ID NOS: 86
 ; SEQ ID NO 15
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-09-256-496-15

Query Match 65.7%; Score 13.8; DB 2; Length 18;
 Best Local Similarity 88.2%; Pred. No. 7.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGCTCTTCA 17
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 Db 1 CAGCAGCAGGATCTTCA 17

RESULT 14

US-08-467-603-54/c
 ; Sequence 54, Application US/08467603
 ; Patent No. 5843672
 ; GENERAL INFORMATION:

APPLICANT: Morgenstern, Jay P.
 APPLICANT: Kanieczny, Andrzej
 APPLICANT: Bizindaukas, Christine B.
 APPLICANT: Brauer, Andrew W.
 TITLE OF INVENTION: Allergenic Proteins and
 TITLE OF INVENTION: Peptides from Dog
 TITLE OF INVENTION: Dander and Uses Therefor
 NUMBER OF SEQUENCES: 104
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 State Street, suite 510
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII-text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,603
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/156,549
 FILING DATE:
 APPLICATION NUMBER: 07/999,712
 FILING DATE: 31-Dec-92
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragouras, Amy E.
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: IMI-0266CP(IPC-048CP)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 INFORMATION FOR SEQ ID NO: 54:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 37 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 US-08-467-603-54

Query Match 65.7%; Score 13.8; DB 2; Length 37;
 Best Local Similarity 88.2%; Pred. No. 8.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCAGCAGAGCTCTTCAT 18
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 Db 30 AGGAGCAGGCTCTTCAT 14

RESULT 15

US-08-466-793-54/c
 ; Sequence 54, Application US/08466793
 ; Patent No. 5891716
 ; GENERAL INFORMATION:
 ; APPLICANT: Morgenstern, Jay P.
 ; APPLICANT: Kanieczny, Andrzej
 ; APPLICANT: Bizindaukas, Christine B.
 ; APPLICANT: Brauer, Andrew W.
 TITLE OF INVENTION: Allergenic Proteins and
 TITLE OF INVENTION: Peptides from Dog
 TITLE OF INVENTION: Dander and Uses Therefor
 NUMBER OF SEQUENCES: 104
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 State Street, suite 510
 CITY: Boston
 STATE: MA
 COUNTRY: USA

ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII-text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,793
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/156,549
FILING DATE: 22-NOV-1993
APPLICATION NUMBER: 07/999,712
FILING DATE: 31-Dec-92
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-026CP(IPC-048CP)
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-466-793-54

Query Match 65.78; Score 13.8; DB 2; Length 37;
Best Local Similarity 88.28; Pred. No. 8.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 AGCAGCAGAGTCTTCAT 18
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Db 30 AGGAGCAGGGTCTTCAT 14

Search completed: April 18, 2003, 08:56:37
Job time : 61 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2003, 07:05:10 ; Search time: 1839 Seconds
(without alignments)
332.332 Million cell updates/sec

Title: PCT-US03-05305-4

Perfect score: 21
Sequence: 1 cagcagcagagcttcattcat 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues 841850

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: gb.ba.*
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- 27: em.sts.*
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- 29: em.vi.*
- 30: em.htg_hum.*
- 31: em.htg_inv.*
- 32: em.htg_other.*
- 33: em.htg_mus.*
- 34: em.htg_pln.*
- 35: em.htg_rod.*
- 36: em.htg_mam.*
- 37: em.htg_vrt.*
- 38: em.sv.*
- 39: em.htgo_hum.*
- 40: em.htgo_mus.*
- 41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
C 1	16.2	77.1	48	6	A76301 Sequence 7
C 2	16.2	77.1	48	6	E01067 DNA sequenc
C 3	15.4	73.3	39	6	A08489 B.taurus ge
C 4	15.4	73.3	39	6	A12568 fragment of
C 5	15.4	73.3	45	6	A05116 Oligonucleo
C 6	15.2	72.4	22	6	AX268965 Sequence
C 7	14.8	70.5	27	6	AX118356 Sequence
C 8	14.8	70.5	31	6	AX070079 Sequence
C 9	14.6	69.5	48	6	A76303 Sequence 9
C 10	14.4	68.6	39	6	A08490 oligonucleo
C 11	14.4	68.6	39	6	A08491 oligonucleo
C 12	14.4	68.6	39	6	A12569 fragment of
C 13	14.4	68.6	39	6	A12570 fragment of
C 14	14.2	67.6	20	6	AR085567 Sequence
C 15	14.2	67.6	30	6	A70102 Sequence 20
C 16	14.2	67.6	30	6	AR148235 Sequence
C 17	14.2	67.6	30	6	AR204084 Sequence
C 18	13.8	65.7	18	6	AR092800 Sequence
C 19	13.8	65.7	31	6	A36373 Sequence 6
C 20	13.8	65.7	37	6	AR070094 Sequence
C 21	13.8	65.7	50	6	AX233374 Sequence
C 22	13.6	64.8	50	6	AX080828 Sequence
C 23	13.6	64.8	50	6	AX403425 Sequence
C 24	13.4	63.8	34	6	AR045234 Sequence
C 25	13.4	63.8	34	6	I52286 Sequence 27
C 26	13.2	62.9	18	6	AR085592 Sequence
C 27	13.2	62.9	23	6	AX262444 Sequence
C 28	13.2	62.9	26	6	AX462235 Sequence
C 29	13.2	62.9	31	6	AX249499 Sequence
C 30	13.2	62.9	32	6	AX339313 Sequence
C 31	13.2	62.9	33	6	A36538 Sequence 79
C 32	13.2	62.9	33	6	AR080171 Sequence
C 33	13.2	62.9	34	6	A93582 Sequence 12
C 34	13.2	62.9	34	6	BD012889 Nucleus 1
C 35	13.2	62.9	34	23	BD008324 Nucleus 1
C 36	13.2	62.9	35	6	AX252822 Sequence
C 37	13.2	62.9	38	6	AR204099 Sequence
C 38	13.2	62.9	47	6	AX114377 Sequence
C 39	13.2	62.9	47	6	AX195012 Sequence
C 40	13	61.9	23	6	A91622 Sequence 14
C 41	13	61.9	23	6	I37350 Sequence 36
C 42	13	61.9	23	6	I94200 Sequence 36
C 43	13	61.9	24	6	E29370 Method for
C 44	13	61.9	27	6	BD013293 DNA compr
C 45	13	61.9	27	23	BD010314 DNA compr

ALIGNMENTS

RESULT 1
A76301/c
LOCUS A76301 48 bp DNA linear PAT 19-OCT-1999
DEFINITION Sequence 7 from Patent WO9319173.
ACCESSION A76301
VERSION A76301.1 GI:6088388
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 48)
AUTHORS Maegert, H.
TITLE DNA CODING FOR APHRODISIN
JOURNAL Patent: WO 9319173-A 7 30-SEP-1993;
FORSSMANN WOLF GEORG (DE)

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FEATURES
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    Location/Qualifiers
      1..48
        /organism="unidentified"
        /db_xref="taxon:32644"
      1..>48
        /note="unnamed protein product"
        /codon_start=1
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        /db_xref="GI:6088389"
        /translation="MKILLALLVFLAHA"
  BASE COUNT
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  ORIGIN
    Query Match 77.1%; Score 16.2; DB 6; Length 48;
    Best Local Similarity 85.7%; Pred. No. 5.1e+03;
    Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
  QY 1 CAGCAGCAGAGTCTTCATCAT 21
    ||||| ||||| ||||| |||||
  Db 21 CAGCAGCAGAGTCTTCATCAT 1

RESULT 2
LOCUS E01067/c 48 bp DNA linear PAT 29-SEP-1997
DEFINITION DNA sequence coding for human pancreas-2 signal peptide.
ACCESSION E01067
VERSION E01067.1 GI:2169326
KEYWORDS JP 1987000276-A/9.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 48)
  Takiguchi,H., Furukawa,H. and Tani,T.
  PRODUCTION OF PANCREAS ELASTASE
  Patent: JP 1987000276-A 9 06-JAN-1987;
  SANKYO CO LTD NIPPON SODA CO LTD, NISSAN CHEM IND LTD, TOYO SODA
  MFG CO LTD
  OS homo sapiens (human)
  PN JP 1987000276-A/9
  PD 06-JAN-1987
  PF 25-JUN-1985 JP 1985138494
  PI TAKIGUCHI HIROSHI, FURUKAWA HIDEHIKO, TANI TOKIO PC
  C12N9/66,A61K35/74,A61K37/54,C12N15/00/C07H21/04,(C12N9/66, PC
  C12R1:19),
  PC (C12N15/00,C12R1:19);
  CC strandedness: Double;
  CC topology: Linear;
  CC hypothetical: No;
  CC anti-sense: No;
  CC *source: tissue_type=pancreas;
  FH key
  FT sig_peptide
  FT 1..48
    /product='human pancreas elastase-2 signal
    peptide'.
  FT
  FEATURES
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      Location/Qualifiers
        1..48
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          /db_xref="taxon:9606"
        7 a 13 c 14 g 14 t
  BASE COUNT
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    Query Match 77.1%; Score 16.2; DB 6; Length 48;
    Best Local Similarity 85.7%; Pred. No. 5.1e+03;
    Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
  QY 1 CAGCAGCAGAGTCTTCATCAT 21
    ||||| ||||| ||||| |||||
  Db 21 CAGCAGCAGAGTCTTCATCAT 1

RESULT 3
LOCUS A08489 39 bp DNA linear PAT 22-JUL-1993
DEFINITION B.taurus gene for somatotropin, partial.
ACCESSION A08489
VERSION A08489.1 GI:410773
KEYWORDS somatotropin.
SOURCE Bos taurus.
ORGANISM Bos taurus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
  Bovinae; Bos.
  1 (bases 1 to 39)
  Harbour,G.C., Hoogerheide,J.G. and Garlick,R.L.
  Enhanced bioactivity of mammalian somatotropin through selective
  deamidation
  Patent: EP 0263206-A 5 13-APR-1988;
  THE UPJOHN COMPANY
  Location/Qualifiers
    1..39
      /organism="Bos taurus"
      /db_xref="taxon:9913"
      <1..>39
      /codon_start=1
      /product="somatotropin"
      /protein_id="CAA00787.1"
      /db_xref="GI:410774"
      /db_xref="SWISS-PROT:P01246"
      /translation="LQFLSRVFTNSLV"
  BASE COUNT
    8 a 12 c 9 g 10 t
  ORIGIN
    Query Match 73.3%; Score 15.4; DB 6; Length 39;
    Best Local Similarity 94.1%; Pred. No. 1.3e+04;
    Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
  QY 4 CAGCAGAGTCTTCATCA 20
    ||||| ||||| ||||| |||||
  Db 12 CAGCAGAGTCTTCACCA 28

RESULT 4
LOCUS A12568 39 bp DNA linear PAT 04-JAN-1994
DEFINITION fragment of bovine somatotropin.
ACCESSION A12568
VERSION A12568.1 GI:488953
KEYWORDS
SOURCE Bos taurus.
ORGANISM Bos taurus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
  Bovinae; Bos.
  1..39
    Location/Qualifiers
      1..39
        /organism="Bos taurus"
        /db_xref="taxon:9913"
  BASE COUNT
    8 a 13 c 8 g 10 t
  ORIGIN
    Query Match 73.3%; Score 15.4; DB 6; Length 39;
    Best Local Similarity 94.1%; Pred. No. 1.3e+04;
    Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
  QY 4 CAGCAGAGTCTTCATCA 20
    ||||| ||||| ||||| |||||
  Db 12 CAGCAGAGTCTTCACCA 28

RESULT 5
LOCUS A05116 45 bp DNA linear PAT 04-MAY-1993
DEFINITION Oligonucleotide U7 for bovine growth hormone.
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ACCESSION A05116
VERSION A05116.1 GI:345003
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
FEATURES
    source
        1..45
            Location/Qualifiers
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                /db_xref="taxon:32630"
BASE COUNT 8 a 17 c 10 g 10 t
ORIGIN
Query Match 73.3%; Score 15.4; DB 6; Length 45;
Best Local Similarity 94.1%; Pred. No. 1.2e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCAGAGTCTTCATCA 20
||||| ||| |||
Db 21 CAGCAGAGTCTTCACCA 37

RESULT 6
AX268965
LOCUS AX268965 22 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 46 from Patent WO0175165.
ACCESSION AX268965
VERSION AX268965.1 GI:16541984
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
artificial sequences.
REFERENCE
AUTHORS Mcconlogue,L.C., Games,K.D., Yednock,T.A., Hua,T., Messersmith,E.
and Bard,F.
TITLE Screening markers and methods for neurodegenerative disorders
JOURNAL Patent: WO 0175165-A 46 11-OCT-2001;
Elan Pharmaceuticals, Inc. (US)
FEATURES
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            /note="forward primer 662F"
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ORIGIN

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Best Local Similarity 85.0%; Pred. No. 1.6e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCA 20
||||| ||| ||| ||| |||
Db 2 CAGCACCAGTCTTCATCA 21

RESULT 7
AX118356/c
LOCUS AX118356 27 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 3479 from Patent WO0129262.
ACCESSION AX118356
VERSION AX118356.1 GI:14035307
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
artificial sequences.
REFERENCE
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 3479 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES
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misc_feature
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ORIGIN

Query Match 70.5%; Score 14.8; DB 6; Length 27;
Best Local Similarity 84.2%; Pred. No. 2.5e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGCAGCAGAGTCTTCATCA 20
||||| ||| ||| |||
Db 22 AGCAGCAGTGTGTNCATCA 4

RESULT 8
AR070079/c
LOCUS AR070079 31 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 35 from patent US 5891716.
ACCESSION AR070079
VERSION AR070079.1 GI:7220967
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE
AUTHORS 1 (bases 1 to 31)
Morgenstern,J.P., Konieczny,A., Bizinkauskas,C.B. and Brauer,A.W.
TITLE Allergenic proteins and peptides from dog dander and use therefor
JOURNAL Patent: US 5891716-A 35 06-APR-1999;
FEATURES
    Location/Qualifiers
        source
            1..31
                /organism="unknown"
BASE COUNT 7 a 13 c 5 g 6 t
ORIGIN

Query Match 70.5%; Score 14.8; DB 6; Length 31;
Best Local Similarity 88.9%; Pred. No. 2.5e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCAGCAGAGTCTTCATC 19
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Db 24 AGGAGCAGGGTCTTCATC 7

RESULT 9
A76303/c
LOCUS A76303 48 bp DNA linear PAT 19-OCT-1999
DEFINITION Sequence 9 from Patent WO9319173.
ACCESSION A76303
VERSION A76303.1 GI:6088390
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
Unclassified.
REFERENCE
AUTHORS 1 (bases 1 to 48)
Maegert,H.
TITLE DNA CODING FOR APHRODISIN
JOURNAL Patent: WO 9319173-A 9 30-SEP-1993;
FORSSMANN WOLF GEORG (DE)
FEATURES
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BASE COUNT 7 a 8 c 14 g 19 t
ORIGIN

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Query Match      69.5%; Score 14.6; DB 6; Length 48;
Best Local Similarity 81.0%; Pred. No. 3e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
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Db 21 CAGCACCAGAGTCTTTACCAT 1

RESULT 10
A08490
LOCUS      A08490          39 bp      DNA      linear      PAT 22-JUL-1993
DEFINITION oligonucleotide 3.
ACCESSION  A08490
VERSION    A08490.1 GI:413472
KEYWORDS   .
SOURCE     synthetic construct.
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 39)
AUTHORS    Harbour,G.C., Hoogerheide,J.G. and Garlick,R.L.
TITLE      Enhanced bioactivity of mammalian somatotropin through selective
JOURNAL    deamidation
PATENT:    EP 0263206-A 6 13-APR-1988;
THE UPJOHN COMPANY
FEATURES    Location/Qualifiers
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BASE COUNT  7 a 12 c 10 g 10 t
ORIGIN

Query Match      68.6%; Score 14.4; DB 6; Length 39;
Best Local Similarity 93.8%; Pred. No. 3.8e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCAGAGTCTTCATC 19
||||| ||||| ||||| |||||
Db 12 CAGCAGAGTCTTCACC 27

RESULT 11
A08491
LOCUS      A08491          39 bp      DNA      linear      PAT 22-JUL-1993
DEFINITION oligonucleotide 4.
ACCESSION  A08491
VERSION    A08491.1 GI:413473
KEYWORDS   .
SOURCE     synthetic construct.
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 39)
AUTHORS    Harbour,G.C., Hoogerheide,J.G. and Garlick,R.L.
TITLE      Enhanced bioactivity of mammalian somatotropin through selective
JOURNAL    deamidation
PATENT:    EP 0263206-A 7 13-APR-1988;
THE UPJOHN COMPANY
FEATURES    Location/Qualifiers
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BASE COUNT  8 a 11 c 10 g 10 t
ORIGIN

Query Match      68.6%; Score 14.4; DB 6; Length 39;
Best Local Similarity 93.8%; Pred. No. 3.8e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCAGAGTCTTCATC 19
||||| ||||| ||||| |||||
Db 12 CAGCAGAGTCTTCACC 27

RESULT 12
A12569
LOCUS      A12569          39 bp      DNA      linear      PAT 04-JAN-1994
DEFINITION fragment of synthetic somatotropin.
ACCESSION  A12569
VERSION    A12569.1 GI:491409
KEYWORDS   .
SOURCE     synthetic construct.
ORGANISM   artificial sequences.
FEATURES    Location/Qualifiers
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            /db_xref="taxon:32630"
BASE COUNT  7 a 12 c 10 g 10 t
ORIGIN

Query Match      68.6%; Score 14.4; DB 6; Length 39;
Best Local Similarity 93.8%; Pred. No. 3.8e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCAGAGTCTTCATC 19
||||| ||||| ||||| |||||
Db 12 CAGCAGAGTCTTCACC 27

RESULT 13
A12570
LOCUS      A12570          39 bp      DNA      linear      PAT 04-JAN-1994
DEFINITION fragment of synthetic somatotropin.
ACCESSION  A12570
VERSION    A12570.1 GI:491410
KEYWORDS   .
SOURCE     synthetic construct.
ORGANISM   artificial sequences.
FEATURES    Location/Qualifiers
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            /db_xref="taxon:32630"
BASE COUNT  8 a 11 c 10 g 10 t
ORIGIN

Query Match      68.6%; Score 14.4; DB 6; Length 39;
Best Local Similarity 93.8%; Pred. No. 3.8e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAGCAGAGTCTTCATC 19
||||| ||||| ||||| |||||
Db 12 CAGCAGAGTCTTCACC 27

RESULT 14
A085567
LOCUS      A085567          20 bp      DNA      linear      PAT 01-SEP-2000
DEFINITION Sequence 3 from patent US 5981732.
ACCESSION  A085567
VERSION    A085567.1 GI:10012334
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Cowser,L.M.
TITLE      Antisense modulation of G-alpha-13 expression
JOURNAL    Patent: US 5981732-A 3 09-NOV-1999;
FEATURES    Location/Qualifiers
            source
            1..20
            /organism="unknown"
BASE COUNT  5 a 8 c 4 g 3 t
ORIGIN

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 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 30)
 AUTHORS Thompson, A.H. and Schmidt, G.
 TITLE CHARACTERISING DNA
 JOURNAL Patent: WO 9810095-A 20 12-MAR-1998;
 BRAX GENOMICS LTD (GB)
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Search completed: April 18, 2003, 08:26:54
 Job time : 1855 secs

